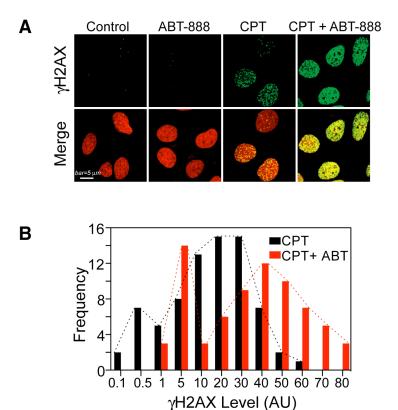
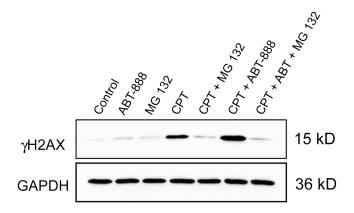


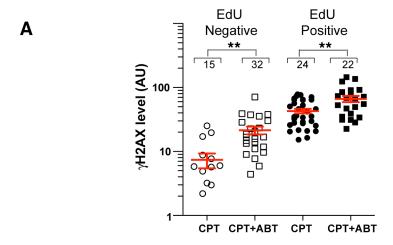
**Supplemental Fig. 1. A.** Fluorescence images of poly(ADP-ribose) (PAR) induction by CPT and suppression by ABT-888 in human osteosarcoma U2OS cells. Cells were treated with 1 μM CPT for 30 min in the absence or presence of ABT-888 (0.5 μM). Nuclei were labeled with PI (red) and PAR polymers are shown in green; Bar = 8 μm. **B.** Clonogenic assays. HT-29 Cells were treated with 1 μM CPT for 30 min in the absence or presence of ABT-888 (0.5 μM). Then drugs were washed away and cells were cultured for 10 days to allow colony formation. The survival fraction of untreated cells was defined as 100%. Data are shown as mean values  $\pm$  S.D.(n = 3 independent experiments). Standard *t*-tests were used for statistical analyses; \*\*p<0.01.

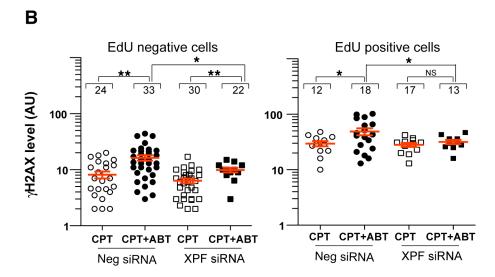


Supplemental Fig. 2. Induction of  $\gamma H2AX$  by ABT-888 in CPT-treated cells. U2OS cells were treated with CPT (1  $\mu M$ ) for 30 min in the presence or absence of ABT-888 (0.5  $\mu M$ ). A. Representative confocal microscope images of  $\gamma H2AX$ ; B. Distribution of  $\gamma H2AX$  levels analyzed through quantitative analysis of  $\gamma H2AX$  signal cell by cell; Dotted curves link the edges of columns (black, CPT; red, CPT+ABT-888).



**Supplemental Fig. 3.** U2OS cells were pre-treated with the proteasome inhibitor MG-132 (10  $\mu$ M for 2 h) before being exposed to CPT (1  $\mu$ M) for 30 min in the presence or absence of ABT-888 (0.5  $\mu$ M).  $\gamma$ H2AX levels were detected by Western blotting.





**Supplemental Fig. 4** Duplicate independent experiments for single cell analyses. **A**. U2OS cells were treated with CPT (1  $\mu$ M) for 30 min in the presence or absence of ABT-888 (0.5  $\mu$ M). **B**. 48 h after transfection with *XPF* siRNAs, U2OS cells were labeled with EdU and treated with CPT (1  $\mu$ M) for 30 min in the absence or presence of ABT-888 (0.5  $\mu$ M). Cells were fixed and stained for immunofluorescence assays. Scattered-dot plots were derived by analyzing the  $\gamma$ H2AX level of individual cells in each experiment. Mean values  $\pm$  S.E.M. are shown as red bars. Numbers above each cluster indicate the number of cells counted. Standard *t*-tests were used for statistical analyses ,\*\* p<0.01; \* p<0.05; *NS*, no significant difference.